

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number:

10/524,970

Source:

PCT

Date Processed by STIC:

2-26-05

ENTERED



PCT

RAW SEQUENCE LISTING

DATE: 02/26/2005

PATENT APPLICATION: US/10/524,970

TIME: 08:09:35

Input Set : A:\pto.da.txt

Output Set: N:\CRF4\02262005\J524970.raw

```

3 <110> APPLICANT: SUMITOMO CORPORATION
4   Irimura, Tatsuro
6 <120> TITLE OF INVENTION: Use of Lectin Library for glycoprotein and cell
identification, serum and
7   cell diagnosis, and glycoprotein and cell fractionization
9 <130> FILE REFERENCE: SAP-702-PCT
C--> 11 <140> CURRENT APPLICATION NUMBER: US/10/524,970
C--> 11 <141> CURRENT FILING DATE: 2005-02-18
11 <150> PRIOR APPLICATION NUMBER: JP2002-239979
12 <151> PRIOR FILING DATE: 2002-08-20
14 <160> NUMBER OF SEQ ID NOS: 31
16 <170> SOFTWARE: PatentIn version 3.1
18 <210> SEQ ID NO: 1
19 <211> LENGTH: 950
20 <212> TYPE: DNA
21 <213> ORGANISM: Maackia amurensis
23 <220> FEATURE:
24 <221> NAME/KEY: CDS
25 <222> LOCATION: (4)..(858)
26 <223> OTHER INFORMATION:
W--> 28 <400> 1
29 gcc atg gct act tcc aac tca aaa cca act caa gtc ctt ctt gcc acc      48
30   Met Ala Thr Ser Asn Ser Lys Pro Thr Gln Val Leu Leu Ala Thr
31   1          5          10          15
33 ttc tta act ttc ttc ctt ttg cta ctc aac aac gta aac tca tca gat      96
34 Phe Leu Thr Phe Phe Leu Leu Leu Leu Asn Asn Val Asn Ser Ser Asp
35   20          25          30
37 gag ctt tct ttt acc atc aac aat ttc atg cca aat caa ggc gat cta      144
38 Glu Leu Ser Phe Thr Ile Asn Asn Phe Met Pro Asn Gln Gly Asp Leu
39   35          40          45
41 ctc ttc caa ggt gta gcc act gtt tca cca aca ggg gta tta caa ctt      192
42 Leu Phe Gln Gly Val Ala Thr Val Ser Pro Thr Gly Val Leu Gln Leu
43   50          55          60
45 acc agc gaa gaa aac ggt caa ccc ctg gag tat tct gtt ggc aga gct      240
46 Thr Ser Glu Glu Asn Gly Gln Pro Leu Glu Tyr Ser Val Gly Arg Ala
47   65          70          75
49 cta tat act gcc cct gtg cgc att tgg gac agt acc act ggc gcc gta      288
50 Leu Tyr Thr Ala Pro Val Arg Ile Trp Asp Ser Thr Thr Gly Ala Val
51 80          85          90          95
53 gca agc ttc tcc act tcc ttc acc ttt gtt gtg aaa gca gct agg gga      336
54 Ala Ser Phe Ser Thr Ser Phe Thr Phe Val Lys Ala Ala Arg Gly
55   100         105         110
57 gct tct gac ggt tta gcc ttc ttt ctt gca cca cct gat tct cag atc      384
58 Ala Ser Asp Gly Leu Ala Phe Phe Leu Ala Pro Pro Asp Ser Gln Ile

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59          115          120          125
61 cct tcg ggc agc gta tcg aaa tac cta gga ctt ttt aac aac tca aat      432
62 Pro Ser Gly Ser Val Ser Lys Tyr Leu Gly Leu Phe Asn Asn Ser Asn
63          130          135          140
65 tcc gat agt tcc aac caa att gtt gct gta gag ttt gac act tac ttc      480
66 Ser Asp Ser Ser Asn Gln Ile Val Ala Val Glu Phe Asp Thr Tyr Phe
67          145          150          155
69 ggc cat agt tat gat ccc tgg gat cca aat tat cga cat atc gga att      528
70 Gly His Ser Tyr Asp Pro Trp Asp Pro Asn Tyr Arg His Ile Gly Ile
71 160          165          170          175
73 gat gtc aac ggt att gag tcg ata aaa act gtg caa tgg gat tgg att      576
74 Asp Val Asn Gly Ile Glu Ser Ile Lys Thr Val Gln Trp Asp Trp Ile
75          180          185          190
77 aac ggc gga gtt gcc ttt gct acc ata acc tat cta gct ccc aac aaa      624
78 Asn Gly Gly Val Ala Phe Ala Thr Ile Thr Tyr Leu Ala Pro Asn Lys
79          195          200          205
81 acg tta ata gca tct cta gtt tac cct tcc aat caa aca agt ttc att      672
82 Thr Leu Ile Ala Ser Leu Val Tyr Pro Ser Asn Gln Thr Ser Phe Ile
83          210          215          220
85 gtc gct gct tct gtt gat ttg aag gga atc ctc cct gag tgg gtt aga      720
86 Val Ala Ala Ser Val Asp Leu Lys Gly Ile Leu Pro Glu Trp Val Arg
87          225          230          235
89 gtt ggt ttc tct gct gcc acg ggt gct cct aaa gca gtt gaa acc cac      768
90 Val Gly Phe Ser Ala Ala Thr Gly Ala Pro Lys Ala Val Glu Thr His
91 240          245          250          255
93 gat gtt cgt tcc tgg tct ttc acg tca act ttg gaa gcc aac agc cct      816
94 Asp Val Arg Ser Trp Ser Phe Thr Ser Thr Leu Glu Ala Asn Ser Pro
95          260          265          270
97 gct gat gtg gat aat aat gtg cat atc gca cgt tac act gca      858
98 Ala Asp Val Asp Asn Asn Val His Ile Ala Arg Tyr Thr Ala
99          275          280          285
101 tgatctcgtg agctttcgta tgtattaggt gtttatgtaa attaaataaaa aatgacctga      918
103 aataatgggt atcggcgag ctatacaaaa at      950
106 <210> SEQ ID NO: 2
107 <211> LENGTH: 285
108 <212> TYPE: PRT
109 <213> ORGANISM: Maackia amurensis
111 <400> SEQUENCE: 2
113 Met Ala Thr Ser Asn Ser Lys Pro Thr Gln Val Leu Leu Ala Thr Phe
114 1          5          10          15
117 Leu Thr Phe Phe Leu Leu Leu Leu Asn Asn Val Asn Ser Ser Asp Glu
118          20          25          30
121 Leu Ser Phe Thr Ile Asn Asn Phe Met Pro Asn Gln Gly Asp Leu Leu
122          35          40          45
125 Phe Gln Gly Val Ala Thr Val Ser Pro Thr Gly Val Leu Gln Leu Thr
126          50          55          60
129 Ser Glu Glu Asn Gly Gln Pro Leu Glu Tyr Ser Val Gly Arg Ala Leu
130 65          70          75          80
133 Tyr Thr Ala Pro Val Arg Ile Trp Asp Ser Thr Thr Gly Ala Val Ala

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```

134          85          90          95
137 Ser Phe Ser Thr Ser Phe Thr Phe Val Val Lys Ala Ala Arg Gly Ala
138          100          105          110
141 Ser Asp Gly Leu Ala Phe Phe Leu Ala Pro Pro Asp Ser Gln Ile Pro
142          115          120          125
145 Ser Gly Ser Val Ser Lys Tyr Leu Gly Leu Phe Asn Asn Ser Asn Ser
146          130          135          140
149 Asp Ser Ser Asn Gln Ile Val Ala Val Glu Phe Asp Thr Tyr Phe Gly
150 145          150          155          160
153 His Ser Tyr Asp Pro Trp Asp Pro Asn Tyr Arg His Ile Gly Ile Asp
154          165          170          175
157 Val Asn Gly Ile Glu Ser Ile Lys Thr Val Gln Trp Asp Trp Ile Asn
158          180          185          190
161 Gly Gly Val Ala Phe Ala Thr Ile Thr Tyr Leu Ala Pro Asn Lys Thr
162          195          200          205
165 Leu Ile Ala Ser Leu Val Tyr Pro Ser Asn Gln Thr Ser Phe Ile Val
166          210          215          220
169 Ala Ala Ser Val Asp Leu Lys Gly Ile Leu Pro Glu Trp Val Arg Val
170 225          230          235          240
173 Gly Phe Ser Ala Ala Thr Gly Ala Pro Lys Ala Val Glu Thr His Asp
174          245          250          255
177 Val Arg Ser Trp Ser Phe Thr Ser Thr Leu Glu Ala Asn Ser Pro Ala
178          260          265          270
181 Asp Val Asp Asn Asn Val His Ile Ala Arg Tyr Thr Ala
182          275          280          285
185 <210> SEQ ID NO: 3
186 <211> LENGTH: 32
187 <212> TYPE: DNA
188 <213> ORGANISM: Artificial
190 <220> FEATURE:
191 <223> OTHER INFORMATION: Tag Primer pFLAG-Spe I-sense
193 <400> SEQUENCE: 3
194 ccgggtacct gcactagtag atagatgagc tc
197 <210> SEQ ID NO: 4
198 <211> LENGTH: 32
199 <212> TYPE: DNA
200 <213> ORGANISM: Artificial
202 <220> FEATURE:
203 <223> OTHER INFORMATION: Tag Primer pFLAG-Spe I-anti
205 <400> SEQUENCE: 4
206 gagctcatct atctactagt gcagggtaccc gg
209 <210> SEQ ID NO: 5
210 <211> LENGTH: 26
211 <212> TYPE: DNA
212 <213> ORGANISM: Artificial
214 <220> FEATURE:
215 <223> OTHER INFORMATION: pFLAG-XhoI
217 <400> SEQUENCE: 5
218 ccagggtgaaa ctgctcgagt cagatg

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221 <210> SEQ ID NO: 6
222 <211> LENGTH: 28
223 <212> TYPE: DNA
224 <213> ORGANISM: Artificial
226 <220> FEATURE:
227 <223> OTHER INFORMATION: Primer MAH-Spe I-anti
229 <400> SEQUENCE: 6
230 tgggcaacta gttgcagtgt aacgtgcg                28
233 <210> SEQ ID NO: 7
234 <211> LENGTH: 26
235 <212> TYPE: DNA
236 <213> ORGANISM: Artificial
238 <220> FEATURE:
239 <223> OTHER INFORMATION: Analyzing Primer N-26
241 <400> SEQUENCE: 7
242 catcataacg gttctggcaa atattc                26
245 <210> SEQ ID NO: 8
246 <211> LENGTH: 24
247 <212> TYPE: DNA
248 <213> ORGANISM: Artificial
250 <220> FEATURE:
251 <223> OTHER INFORMATION: Sequence Primer Loop D-Seq
253 <400> SEQUENCE: 8
254 gttaatagca tctctagttt accc                24
257 <210> SEQ ID NO: 9
258 <211> LENGTH: 59
259 <212> TYPE: DNA
260 <213> ORGANISM: Artificial
262 <220> FEATURE:
263 <223> OTHER INFORMATION: Inert Primer LLD3
265 <220> FEATURE:
266 <221> NAME/KEY: misc_feature
267 <222> LOCATION: (34)..(35)
268 <223> OTHER INFORMATION: n is a or c or g or t or u.
271 <220> FEATURE:
272 <221> NAME/KEY: misc_feature
273 <222> LOCATION: (33)..(33)
274 <223> OTHER INFORMATION: m is a or c.
277 <400> SEQUENCE: 9
W--> 278 ctacaagatc taacatcgtg ggtttcaact gcmnnntttag gagcaccctg ggcagcaga    59
281 <210> SEQ ID NO: 10
282 <211> LENGTH: 59
283 <212> TYPE: DNA
284 <213> ORGANISM: Artificial
286 <220> FEATURE:
287 <223> OTHER INFORMATION: Insert Primer LLD4
289 <220> FEATURE:
290 <221> NAME/KEY: misc_feature
291 <222> LOCATION: (37)..(38)

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Input Set : A:\pto.da.txt

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292 <223> OTHER INFORMATION: n is a or c or g or t or u.
295 <220> FEATURE:
296 <221> NAME/KEY: misc_feature
297 <222> LOCATION: (36)..(36)
298 <223> OTHER INFORMATION: m is a or c.
301 <400> SEQUENCE: 10
W--> 302 ctacaagatc taacatcgtg gggtttcaact gctttmnag gagcaccgt ggcagcaga 59
305 <210> SEQ ID NO: 11
306 <211> LENGTH: 59
307 <212> TYPE: DNA
308 <213> ORGANISM: Artificial
310 <220> FEATURE:
311 <223> OTHER INFORMATION: Insert Primer LLD5
313 <220> FEATURE:
314 <221> NAME/KEY: misc_feature
315 <222> LOCATION: (40)..(41)
316 <223> OTHER INFORMATION: n is a or c or g or t or u.
319 <220> FEATURE:
320 <221> NAME/KEY: misc_feature
321 <222> LOCATION: (39)..(39)
322 <223> OTHER INFORMATION: m is a or c.
325 <400> SEQUENCE: 11
W--> 326 ctacaagatc taacatcgtg gggtttcaact gctttaggmn nagcaccgt ggcagcaga 59
329 <210> SEQ ID NO: 12
330 <211> LENGTH: 59
331 <212> TYPE: DNA
332 <213> ORGANISM: Artificial
334 <220> FEATURE:
335 <223> OTHER INFORMATION: Insert Primer LLD6
337 <220> FEATURE:
338 <221> NAME/KEY: misc_feature
339 <222> LOCATION: (43)..(44)
340 <223> OTHER INFORMATION: n is a or c or g or t or u.
343 <220> FEATURE:
344 <221> NAME/KEY: misc_feature
345 <222> LOCATION: (42)..(42)
346 <223> OTHER INFORMATION: m is a or c.
349 <400> SEQUENCE: 12
W--> 350 ctacaagatc taacatcgtg gggtttcaact gctttaggag cmnnaccgt ggcagcaga 59
353 <210> SEQ ID NO: 13
354 <211> LENGTH: 59
355 <212> TYPE: DNA
356 <213> ORGANISM: Artificial
358 <220> FEATURE:
359 <223> OTHER INFORMATION: Insert Primer MAH loop D-1 Phe
361 <400> SEQUENCE: 13
362 ctacaagatc taacatcgtg gggtttcaaaa actgcttttag gagcaccgt ggcagcaga 59
365 <210> SEQ ID NO: 14
366 <211> LENGTH: 59

```

RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/10/524,970

DATE: 02/26/2005
TIME: 08:09:36

Input Set : A:\pto.da.txt
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:9; N Pos. 34,35

Seq#:10; N Pos. 37,38

Seq#:11; N Pos. 40,41

Seq#:12; N Pos. 43,44

Invalid Line Length:

The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:1; Line(s) 6

Invalid <213> Response:

Use of "Artificial" only as "<213> Organism" response is incomplete, per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:3,4,5,6,7,8,9,10,11,12,13,14,15,16,17,18,19,20,21,22,23,24,25,26,27,28,29

Seq#:30,31

VERIFICATION SUMMARY

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Input Set : A:\pto.da.txt

Output Set: N:\CRF4\02262005\J524970.raw

L:11 M:270 C: Current Application Number differs, Replaced Current Application No
L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:28 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:1,Line#:26
L:278 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9 after pos.:0
L:302 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10 after pos.:0
L:326 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11 after pos.:0
L:350 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12 after pos.:0